

RAW SEQUENCE LISTING  
PATENT APPLICATION US/10/023,775

DATE: 01/17/2002  
TIME: 06:51:31

INPUT SET: S36722.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

1 GENERAL INFORMATION: SEQUENCE LISTING

2  
3 (1) General Information:

Does Not Comply  
Corrected Diskette Needed

4  
5 (i) APPLICANT: ↑ move up to (i) APPLICANT: line  
6 ~~(A) NAME: Boehringer Mannheim GmbH~~  
7 ~~(B) STREET: Sandhofer Str. 112 132~~  
8 ~~(C) CITY: Mannheim~~  
9 ~~(E) COUNTRY: Germany~~  
10 ~~(F) POSTAL CODE: 68305~~

insert these mandatory  
headers and responses  
for a  
U.S.  
case

11  
12 (ii) TITLE OF INVENTION: Fanconi-gene II

13  
14 (iii) NUMBER OF SEQUENCES: 2

15  
16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: Floppy disk  
18 (B) COMPUTER: IBM PC compatible  
19 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

6.1 CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE:  
(B) STREET:  
(C) CITY:  
(D) STATE:  
(E) COUNTRY:  
(F) ZIP:

21  
22 (vi) CURRENT APPLICATION DATA:

23 (A) APPLICATION NUMBER: US/09/977,801  
24 (B) FILING DATE:

25  
26  
27 (vii) PRIOR APPLICATION DATA:

28 (A) APPLICATION NUMBER: US/09/402,632  
29 (B) FILING DATE:

↓ move down with separate  
headers

30  
31  
32  
33 (2) INFORMATION FOR SEQ ID NO: 1:

34  
35 (i) SEQUENCE CHARACTERISTICS:

36 (A) LENGTH: 1026 base pairs  
37 (B) TYPE: nucleic acid  
38 (C) STRANDEDNESS: both  
39 (D) TOPOLOGY: linear

40  
41 (ix) FEATURE:

42 (A) NAME/KEY: CDS  
43 (B) LOCATION: 256..924

44  
45 (ix) FEATURE:

46 (A) NAME/KEY: CDS

EPO format is  
invalid for U.S.  
cases

# RAW SEQUENCE LISTING PATENT APPLICATION US/10/023,775

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47 (B) LOCATION:430..924  
48  
49 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
50  
51 TTTCACCGTC TAGAGGCATA AGAGGTGAGC CCGTGCTCTT CAGCGGAGAA GATCCCCTAC 60  
52  
53 CTGGCCGCCG GCCACTTTCT GTGGGCCGTG GGGTCCTCAA GGAGACGGCC CTTGGGCTCA 120  
54  
55 GGGGCTGCGT TTCCACACGC GCCTTTCCCA GGGCTCCCGC GCCCGTTCCT GCCTGGCCGC 180  
56  
57 CGGCCGCTCC AACAGCAGCA CAAGGCGGGA CTCAGAACCG GCGTTCAGGG CCGCCAGCGG 240  
58  
59 CCGCGAGGCC CTGAG ATG AGG CTC CAA AGA CCC CGA CAG GCC CCG GCG GGT 291  
60 Met Arg Leu Gln Arg Pro Arg Gln Ala Pro Ala Gly  
61 1 5 10  
62  
63 GGG AGG CGC GCG CCC CGG GGC GGG CGG GGC TCC CCC TAC CGG CCA GAC 339  
64 Gly Arg Arg Ala Pro Arg Gly Gly Arg Gly Ser Pro Tyr Arg Pro Asp  
65 15 20 25  
66  
67  
68 CCG GGG AGA GGC GCG CGG AGG CTG CGA AGG TTC CAG AAG GGC GGG GAG 387  
69 Pro Gly Arg Gly Ala Arg Arg Leu Arg Arg Phe Gln Lys Gly Gly Glu  
70 30 35 40  
71  
72 GGG GCG CCG CGC GCT GAC CCT CCC TGG GCA CCG CTG GGG ACG ATG GCG 435  
73 Gly Ala Pro Arg Ala Asp Pro Pro Trp Ala Pro Leu Gly Thr Met Ala  
74 45 50 55 60  
75  
76 CTG CTC GCC TTG CTG CTG GTC GTG GCC CTA CCG CGG GTG TGG ACA GAC 483  
77 Leu Leu Ala Leu Leu Leu Val Val Ala Leu Pro Arg Val Trp Thr Asp  
78 65 70 75  
79  
80 GCC AAC CYG ACT GCG AGA CAA CGA GAT CCA SAG GAC TCC CAG CGA ACG 531  
81 Ala Asn Xaa Thr Ala Arg Gln Arg Asp Pro Xaa Asp Ser Gln Arg Thr  
82 80 85 90  
83  
84 GAC GAG GGT GAC AAT AGA GTG TGG TGT CAT GTT TGT GAG AGA GAA AAC 579  
85 Asp Glu Gly Asp Asn Arg Val Trp Cys His Val Cys Glu Arg Glu Asn  
86 95 100 105  
87  
88 ACT TTC GAG TGC CAG AAC CCA AGG AGG TGC AAA TGG ACA GAG CCA TAC 627  
89 Thr Phe Glu Cys Gln Asn Pro Arg Arg Cys Lys Trp Thr Glu Pro Tyr  
90 110 115 120  
91  
92 TGC GTT ATA GCG GCC GTG AAA ATA TTT CCA CGT TTT TTC ATG GTT GCG 675  
93 Cys Val Ile Ala Ala Val Lys Ile Phe Pro Arg Phe Phe Met Val Ala  
94 125 130 135 140  
95  
96 AAG CAG TGC TCC GCT GGT TGT GCA GCG ATG GAG AGA CCC AAG CCA GAG 723  
97 Lys Gln Cys Ser Ala Gly Cys Ala Ala Met Glu Arg Pro Lys Pro Glu  
98 145 150 155  
99

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100  GAG AAG CGG TTT CTC CTG GAA GAG CCC ATG CCC TTC TTT TAC CTC AAG      771
101  Glu Lys Arg Phe Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr Leu Lys
102                160                      165                      170
103
104  TGT TGT AAA ATT CGC TAC TGC AAT TTA GAG GGG CCA CCT ATC AAC TCA      819
105  Cys Cys Lys Lys Ile Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser
106                175                      180                      185
107
108  TCA GTG TTC AAA GAA TAT GCT GGG AGC ATG GGT GAG AGC TGT GGT GGG      867
109  Ser Val Phe Lys Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly
110                190                      195                      200
111
112  CTG TGG CTG GCC ATC CTC CTG CTG CTG GCC TCC ATT GCA GCC GGC CTC      915
113  Leu Trp Leu Ala Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu
114  205                210                      215                      220
115
116  AGC CTG TCT TGAGCCACGG GACTGCCACA GACTGAGCCT TCCGGAGCAT      964
117  Ser Leu Ser
118
119
120  GGACTCGCTC CAGACCGTTG TCACCTGTTG CATTAAACTT GTTTTCTGTT GAAAAAAAAA 1024
121
122  AA      1026
123
124
125  (2) INFORMATION FOR SEQ ID NO: 2:
126
127      (i) SEQUENCE CHARACTERISTICS:
128          (A) LENGTH: 223 amino acids
129          (B) TYPE: amino acids
130          (D) TOPOLOGY: linear
131
132      (ii) MOLECULE TYPE: protein
133
134      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
135
136
137  Met Arg Leu Gln Arg Pro Arg Gln Ala Pro Ala Gly Gly Arg Arg Ala
138      1                5                10                15
139
140  Pro Arg Gly Gly Arg Gly Ser Pro Tyr Arg Pro Asp Pro Gly Arg Gly
141                20                25                30
142
143  Ala Arg Arg Leu Arg Arg Phe Gln Lys Gly Gly Glu Gly Ala Pro Arg
144                35                40                45
145
146  Ala Asp Pro Pro Trp Ala Pro Leu Gly Thr Met Ala Leu Leu Ala Leu
147      50                55                60
148
149  Leu Leu Val Val Ala Leu Pro Arg Val Trp Thr Asp Ala Asn Xaa Thr
150      65                70                75                80
151
152  Ala Arg Gln Arg Asp Pro Xaa Asp Ser Gln Arg Thr Asp Glu Gly Asp

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	85	90	95
153			
154			
155	Asn Arg Val Trp Cys His Val Cys Glu Arg Glu Asn Thr Phe Glu Cys		
156	100	105	110
157			
158	Gln Asn Pro Arg Arg Cys Lys Trp Thr Glu Pro Tyr Cys Val Ile Ala		
159	115	120	125
160			
161	Ala Val Lys Ile Phe Pro Arg Phe Phe Met Val Ala Lys Gln Cys Ser		
162	130	135	140
163			
164	Ala Gly Cys Ala Ala Met Glu Arg Pro Lys Pro Glu Glu Lys Arg Phe		
165	145	150	155
166			
167	Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr Leu Lys Cys Cys Lys Ile		
168	165	170	175
169			
170	Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys		
171	180	185	190
172			
173	Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala		
174	195	200	205
175			
176	Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser		
177	210	215	220
178			
179			
180			
181			

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/10/023,775**DATE: 01/17/2002  
TIME: 06:51:33**INPUT SET: S36722.raw**

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Boehringer Mannheim GmbH
7	Unknown or Misplaced Identifier	(B) STREET: Sandhofer Str. 112-132
8	Unknown or Misplaced Identifier	(C) CITY: Mannheim
9	Unknown or Misplaced Identifier	(E) COUNTRY: Germany
10	Unknown or Misplaced Identifier	(F) POSTAL CODE: 68305
23	Wrong application Serial Number	(A) APPLICATION NUMBER:US/09/977,801

PAGE: 1

**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/10/023,775**

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TIME: 06:51:33

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ADDRESSEE  
STREET  
CITY  
STATE  
COUNTRY  
ZIP  
CORRESPONDENCE ADDRESS  
CLASSIFICATION